SEQUENCE LISTING

<110> Vannuffel, Pascal
     Gala, Jean-Luc

<120> GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES
FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS

<130> VANM145.001A
<140> 09/509,234
<141> 1998-09-28

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<170> PatentIn version 3.0

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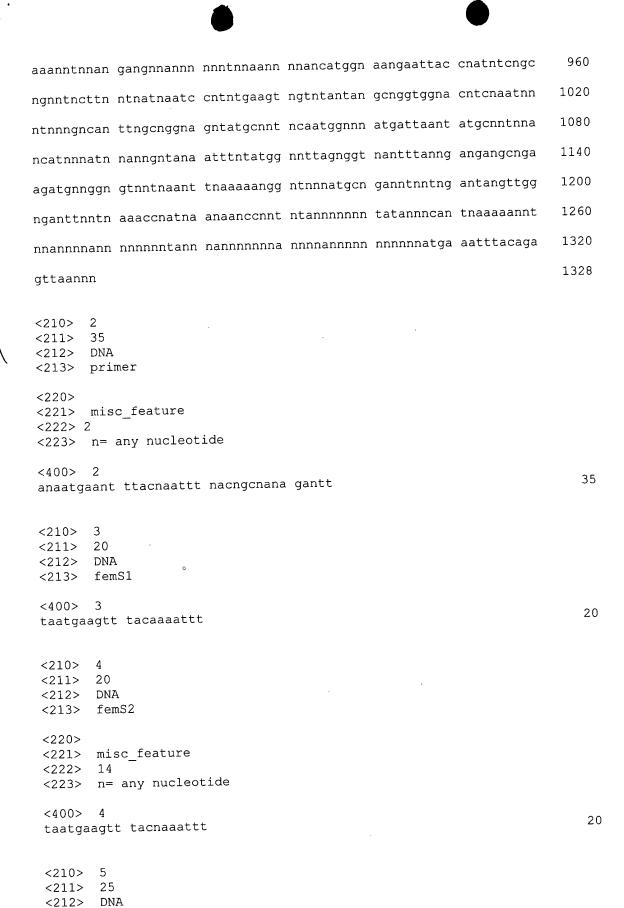<212> DNA
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ggatngnntn ngnaanngna anacnaaaaa agtnnanaan aatggngtna aagtnnnntt   600

nntnnnnnaa ganganntnc cnatnttnng ntcattnatg gangatacnn cnganncnaa   660

ngnnttnnnn gatngngang annnnttnta ntanaanngn tnnnnnnatt nnaaagannn   720

ngtnntngtn ccnntngcnt atatnnantt tgatgantan ntnnnngaan tnnannnnga   780

nngnnannnn ntnantaaag annnnaanaa agcnntnaan ganatngana aangnccnga   840

naanaaaaan gcnnnnaana annnnnnnaa nntnnaanan caantnnnng cnaannanca   900

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ntnnngncan ttngcnggna gntatgcnnt ncaatggnnn atgattaant atgcnntnna     1080

ncatnnnatn nanngntana atttntatgg nnttagnggt nantttanng angangcnga     1140

agatgnnggn gtnntnaant tnaaaaangg ntnnnatgcn ganntnntng antangttgg     1200

nganttnntn aaaccnatna anaanccnnt ntannnnnnn tatannncan tnaaaaannt     1260

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    Met Lys Phe Thr Asn Leu Thr Ala Thr Glu Phe Gly Asn Tyr Thr
    1               5                   10                  15

gat aag atg cca tat agt cat ttc aca caa atg act gaa aac tat gag       96
Asp Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu
                20                  25                  30

atg aaa gtt gca aat aaa aca gaa act cac tta gtt ggt ata aaa aat      144
Met Lys Val Ala Asn Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn
            35                  40                  45
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9

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aaa gat aat gag gtt att gca gcc tgc atg ttg aca gca gta cca gtc        192
Lys Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val
        50                  55                  60

atg aaa ttt ttt aag tac ttt tat tct aac cga gga cct gta att gat        240
Met Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp
        65                  70                  75

tat gat aat aga gag ctt gtt cac ttt ttc ttt aat gag tta aca aag        288
Tyr Asp Asn Arg Glu Leu Val His Phe Phe Phe Asn Glu Leu Thr Lys
80                  85                  90                  95

tat tta aaa cag cat aat tgt cta tat gtt cga gtt gac cct tat tta        336
Tyr Leu Lys Gln His Asn Cys Leu Tyr Val Arg Val Asp Pro Tyr Leu
                100                 105                 110

cca tat caa tat tta aat cat gat ggt gaa att aca ggt aat gct ggt        384
Pro Tyr Gln Tyr Leu Asn His Asp Gly Glu Ile Thr Gly Asn Ala Gly
                115                 120                 125

aat gat tgg ttc ttt gat aag atg aag cat ctc gga ttt gaa cat gaa        432
Asn Asp Trp Phe Phe Asp Lys Met Lys His Leu Gly Phe Glu His Glu
                130                 135                 140

ggc ttt act aaa ggt ttt gat ccg att aaa caa atc cga tat cat tct        480
Gly Phe Thr Lys Gly Phe Asp Pro Ile Lys Gln Ile Arg Tyr His Ser
        145                 150                 155

gtt tta gat tta aaa aat aaa aca tct aaa gat ata tta aat gga atg        528
Val Leu Asp Leu Lys Asn Lys Thr Ser Lys Asp Ile Leu Asn Gly Met
160                 165                 170                 175

gat agt cta cgt aaa cgt aat act aaa aaa gtt caa aaa aat ggt gtg        576
Asp Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val
                180                 185                 190

aaa gtt aag ttc tta tca gaa gaa gaa ctt cca atc ttc cgt tca ttt        624
Lys Val Lys Phe Leu Ser Glu Glu Glu Leu Pro Ile Phe Arg Ser Phe
                195                 200                 205

atg gaa gat aca acc gaa acg aaa gaa ttc caa gat aga gat gat agt        672
Met Glu Asp Thr Thr Glu Thr Lys Glu Phe Gln Asp Arg Asp Asp Ser
        210                 215                 220

ttc tat tat aat cgc tat aga cat ttc aaa gat cac gtg ctt gta cca        720
Phe Tyr Tyr Asn Arg Tyr Arg His Phe Lys Asp His Val Leu Val Pro
        225                 230                 235

cta gct tat att aag ttt gat gag tac atc gaa gaa tta caa aat gaa        768
Leu Ala Tyr Ile Lys Phe Asp Glu Tyr Ile Glu Glu Leu Gln Asn Glu
240                 245                 250                 255

cgt gaa act tta aat aaa gat gtt aat aaa gct tta aaa gat att gaa        816
Arg Glu Thr Leu Asn Lys Asp Val Asn Lys Ala Leu Lys Asp Ile Glu
                260                 265                 270

aaa cga cca gac aat aaa aag gca ttt aat aaa aaa gaa aat ctt gaa        864
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10

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              Lys Arg Pro Asp Asn Lys Lys Ala Phe Asn Lys Lys Glu Asn Leu Glu
                      275                 280                 285

aaa caa tta gat gcc aat caa caa aaa tta gac gag gct aaa aaa tta          912
Lys Gln Leu Asp Ala Asn Gln Gln Lys Leu Asp Glu Ala Lys Lys Leu
        290                 295                 300

caa gcc gaa cat ggt aat gaa tta cca att tca gca ggt ttc ttc ttt         960
Gln Ala Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe
        305                 310                 315

att aat cca ttt gaa gtt gtt tat tat gca ggt gga act tct aat aaa        1008
Ile Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys
320                 325                 330                 335

tat aga cat ttt gca ggc agt tat gct att caa tgg aca atg att aac        1056
Tyr Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Thr Met Ile Asn
                340                 345                 350

tat gca att gat cat ggt att gat aga tac aat ttc tat ggt att agc        1104
Tyr Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser
                355                 360                 365

ggt aat ttt agt gaa gac gct gaa gat gtt gga gtc att aaa ttt aaa        1152
Gly Asn Phe Ser Glu Asp Ala Glu Asp Val Gly Val Ile Lys Phe Lys
                370                 375                 380

aaa ggt ttc aat gca gac gta att gag tat gtt gga gac ttt gtg aaa        1200
Lys Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys
385                 390                 395

cct att aac aaa cct ttg tat tca gtg tat aag aca ctc aaa aag att        1248
Pro Ile Asn Lys Pro Leu Tyr Ser Val Tyr Lys Thr Leu Lys Lys Ile
400                 405                 410                 415

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Lys Lys Arg Phe Asn
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Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu Met
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11

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Lys Val Ala Asn Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn Lys
        35              40                  45

Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val Met
        50              55                  60

Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr
65              70              75                      80

Asp Asn Arg Glu Leu Val His Phe Phe Phe Asn Glu Leu Thr Lys Tyr
            85              90                  95

Leu Lys Gln His Asn Cys Leu Tyr Val Arg Val Asp Pro Tyr Leu Pro
            100             105             110

Tyr Gln Tyr Leu Asn His Asp Gly Glu Ile Thr Gly Asn Ala Gly Asn
        115             120                 125

Asp Trp Phe Phe Asp Lys Met Lys His Leu Gly Phe Glu His Glu Gly
    130             135                 140

Phe Thr Lys Gly Phe Asp Pro Ile Lys Gln Ile Arg Tyr His Ser Val
145             150                 155                 160

Leu Asp Leu Lys Asn Lys Thr Ser Lys Asp Ile Leu Asn Gly Met Asp
            165                 170                 175

Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val Lys
            180                 185                 190

Val Lys Phe Leu Ser Glu Glu Glu Leu Pro Ile Phe Arg Ser Phe Met
        195             200                 205

Glu Asp Thr Thr Glu Thr Lys Glu Phe Gln Asp Arg Asp Asp Ser Phe
    210             215                 220

Tyr Tyr Asn Arg Tyr Arg His Phe Lys Asp His Val Leu Val Pro Leu
225             230                 235                 240

Ala Tyr Ile Lys Phe Asp Glu Tyr Ile Glu Glu Leu Gln Asn Glu Arg
            245             250                 255

Glu Thr Leu Asn Lys Asp Val Asn Lys Ala Leu Lys Asp Ile Glu Lys
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12

Arg Pro Asp Asn Lys Lys Ala Phe Asn Lys Lys Glu Asn Leu Glu Lys
        275   280   285

Gln Leu Asp Ala Asn Gln Gln Lys Leu Asp Glu Ala Lys Lys Leu Gln
        290   295   300

Ala Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe Ile
305   310   315   320

Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys Tyr
                325   330   335

Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Thr Met Ile Asn Tyr
                340   345   350

Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly
        355   360   365

Asn Phe Ser Glu Asp Ala Glu Asp Val Gly Val Ile Lys Phe Lys Lys
        370   375   380

Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys Pro
385   390   395   400

Ile Asn Lys Pro Leu Tyr Ser Val Tyr Lys Thr Leu Lys Lys Ile Lys
                405   410   415

Lys Arg Phe Asn
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1   5   10   15

13

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ttt act caa atg aca ggt aac tat aat tta aaa gtt gcc gaa aaa aca        96
Phe Thr Gln Met Thr Gly Asn Tyr Asn Leu Lys Val Ala Glu Lys Thr
        20                  25                  30

gaa aca cat tta gtt ggt gtt aaa aat aat aat aac gaa gta att gca       144
Glu Thr His Leu Val Gly Val Lys Asn Asn Asn Asn Glu Val Ile Ala
        35                  40                  45

gca tgt tta ttg aca gct gta cca gtc atg aag ttt ttt aaa tac ttt      192
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
    50                  55                  60

tac agc aat aga ggc cca gtt ata gat tat gct aac caa gaa ctt gta      240
Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Ala Asn Gln Glu Leu Val
65                  70                  75                  80

cat ttt ttc ttt aat gag cta act aaa tat tta aaa aag tat aac tgt      288
His Phe Phe Phe Asn Glu Leu Thr Lys Tyr Leu Lys Lys Tyr Asn Cys
                85                  90                  95

ctc tat gtc cgc ata gat cca tac tta cct tat caa tat aga gac cat      336
Leu Tyr Val Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Tyr Arg Asp His
            100                 105                 110

gac ggt aat ata acg gca aat gct ggc aat gat tgg ttt ttc aat aaa      384
Asp Gly Asn Ile Thr Ala Asn Ala Gly Asn Asp Trp Phe Phe Asn Lys
        115                 120                 125

atg gaa caa ctc gga tac cat cat gat ggc ttt aca aca gga ttt gat      432
Met Glu Gln Leu Gly Tyr His His Asp Gly Phe Thr Thr Gly Phe Asp
    130                 135                 140

cca ata tta caa atc aga ttc cat tct att ctt aat tta aag gat aag      480
Pro Ile Leu Gln Ile Arg Phe His Ser Ile Leu Asn Leu Lys Asp Lys
145                 150                 155                 160

aca gct aaa gat gtt tta aat aat atg gat agt tta cgt aaa aga aat      528
Thr Ala Lys Asp Val Leu Asn Asn Met Asp Ser Leu Arg Lys Arg Asn
                165                 170                 175

acc aaa aaa agt tca aaa aat gga gtc aaa gta aag ttc ctt act gaa      576
Thr Lys Lys Ser Ser Lys Asn Gly Val Lys Val Lys Phe Leu Thr Glu
            180                 185                 190

gaa gaa cta cct atc ttt cgt tca ttt atg gag cag acg tca gaa tct      624
Glu Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Gln Thr Ser Glu Ser
            195                 200                 205

aaa gaa ttc tct gat aga gac gac caa ttt tat tac aat cgg ttt aag      672
Lys Glu Phe Ser Asp Arg Asp Asp Gln Phe Tyr Tyr Asn Arg Phe Lys
    210                 215                 220

tac tat aaa gat agg gtg ctt gtg cct cta gca tat tta aaa ttt gat      720
Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Leu Lys Phe Asp
225                 230                 235                 240

gaa tat ata gaa gaa cta acg aat gaa cga caa act tta gaa aaa gat      768
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14

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Glu Tyr Ile Glu Glu Leu Thr Asn Glu Arg Gln Thr Leu Glu Lys Asp
            245                 250                 255

tta ggc aaa gca ctt aaa gac att gag aaa cga cca gat aac aaa aaa        816
Leu Gly Lys Ala Leu Lys Asp Ile Glu Lys Arg Pro Asp Asn Lys Lys
            260                 265                 270

gct tat aat aaa cga gac aac cta caa caa caa ctc gat gcc aat caa        864
Ala Tyr Asn Lys Arg Asp Asn Leu Gln Gln Gln Leu Asp Ala Asn Gln
            275                 280                 285

caa aag tta aat gag gct aat cag tta caa gcg gaa cac ggt aat gag        912
Gln Lys Leu Asn Glu Ala Asn Gln Leu Gln Ala Glu His Gly Asn Glu
            290                 295                 300

tta cct atc tct gcc ggt ttc ttt att att aat ccg ttt gaa gtt gta        960
Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val
305                 310                 315                 320

tac tac gct gga ggt acc gct aat aaa tat cgt cat ttt gca ggt agt       1008
Tyr Tyr Ala Gly Gly Thr Ala Asn Lys Tyr Arg His Phe Ala Gly Ser
                325                 330                 335

tac gcg gtt cag tgg act atg att aac tat gct atc gaa cac ggc ata       1056
Tyr Ala Val Gln Trp Thr Met Ile Asn Tyr Ala Ile Glu His Gly Ile
            340                 345                 350

gac aga tat aat ttc tac ggc att agt gga aac ttc tca gat gat gct       1104
Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asn Phe Ser Asp Asp Ala
            355                 360                 365

gaa gac gca ggt gtc att cgc ttt aaa aaa ggt tat ggt gca gaa gtg       1152
Glu Asp Ala Gly Val Ile Arg Phe Lys Lys Gly Tyr Gly Ala Glu Val
            370                 375                 380

att gaa tac gtt ggt gat ttt gta aaa cct ata aat aaa cct atg tat       1200
Ile Glu Tyr Val Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Met Tyr
385                 390                 395                 400

aaa ctt tat tca gtg tta aaa cga att caa aat aag cta tag             1242
Lys Leu Tyr Ser Val Leu Lys Arg Ile Gln Asn Lys Leu
                405                 410

aggagaatgg attaattatg aaatttacag agtttaac                          1280


<210>   43
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<212>   PRT
<213>   Staphylococcus lugdunensis femA

<400>   43

Thr Ala Asn Glu Phe Gly Asp Phe Thr Asp Gln Met Pro Tyr Ser His
1               5                   10                  15
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Phe Thr Gln Met Thr Gly Asn Tyr Asn Leu Lys Val Ala Glu Lys Thr
        20                  25                  30

Glu Thr His Leu Val Gly Val Lys Asn Asn Asn Asn Glu Val Ile Ala
        35                  40                  45

Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
    50                  55                  60

Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Ala Asn Gln Glu Leu Val
65                  70                  75                  80

His Phe Phe Phe Asn Glu Leu Thr Lys Tyr Leu Lys Lys Tyr Asn Cys
                85                  90                  95

Leu Tyr Val Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Tyr Arg Asp His
            100                 105                 110

Asp Gly Asn Ile Thr Ala Asn Ala Gly Asn Asp Trp Phe Phe Asn Lys
        115                 120                 125

Met Glu Gln Leu Gly Tyr His His Asp Gly Phe Thr Thr Gly Phe Asp
    130                 135                 140

Pro Ile Leu Gln Ile Arg Phe His Ser Ile Leu Asn Leu Lys Asp Lys
145                 150                 155                 160

Thr Ala Lys Asp Val Leu Asn Asn Met Asp Ser Leu Arg Lys Arg Asn
            165                 170                 175

Thr Lys Lys Ser Ser Lys Asn Gly Val Lys Val Lys Phe Leu Thr Glu
        180                 185                 190

Glu Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Gln Thr Ser Glu Ser
    195                 200                 205

Lys Glu Phe Ser Asp Arg Asp Asp Gln Phe Tyr Tyr Asn Arg Phe Lys
    210                 215                 220

Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Leu Lys Phe Asp
225                 230                 235                 240

Glu Tyr Ile Glu Glu Leu Thr Asn Glu Arg Gln Thr Leu Glu Lys Asp
```

16

Leu Gly Lys Ala Leu Lys Asp Ile Glu Lys Arg Pro Asp Asn Lys Lys
     260   265   270

Ala Tyr Asn Lys Arg Asp Asn Leu Gln Gln Gln Leu Asp Ala Asn Gln
     275   280   285

Gln Lys Leu Asn Glu Ala Asn Gln Leu Gln Ala Glu His Gly Asn Glu
     290   295   300

Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val
305   310   315   320

Tyr Tyr Ala Gly Gly Thr Ala Asn Lys Tyr Arg His Phe Ala Gly Ser
        325   330   335

Tyr Ala Val Gln Trp Thr Met Ile Asn Tyr Ala Ile Glu His Gly Ile
      340   345   350

Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asn Phe Ser Asp Asp Ala
     355   360   365

Glu Asp Ala Gly Val Ile Arg Phe Lys Lys Gly Tyr Gly Ala Glu Val
     370   375   380

Ile Glu Tyr Val Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Met Tyr
385   390   395   400

Lys Leu Tyr Ser Val Leu Lys Arg Ile Gln Asn Lys Leu
       405   410

<210> 44
<211> 1295
<212> DNA
<213> Staphylococcus xylosus femA

<220>
<221> CDS
<222> (1)..(1245)

<400> 44
acg caa aag agt ttg ggt gca ttt tca gat aaa atg cca aat agc cat   48
Thr Gln Lys Ser Leu Gly Ala Phe Ser Asp Lys Met Pro Asn Ser His
1   5   10   15

17

```
ttc acg caa atg gta ggg aat tat gaa ttg aaa att gca gaa agt act        96
Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Ile Ala Glu Ser Thr
            20                  25                  30

gaa aca cat tta gta ggt ata aaa aac aat gat aat gaa gtc att gca       144
Glu Thr His Leu Val Gly Ile Lys Asn Asn Asp Asn Glu Val Ile Ala
            35                  40                  45

gct tgt tta tta act gca gta cca gta atg aaa ttc ttt aag tat ttt       192
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
        50                  55                  60

tat act aat aga ggt ccg gtt ata gat ttt gaa aat aaa gaa tta gtg       240
Tyr Thr Asn Arg Gly Pro Val Ile Asp Phe Glu Asn Lys Glu Leu Val
65                  70                  75                  80

cat tac ttt ttc aat gaa cta tct aaa tat gtg aaa aaa cat aat gcg       288
His Tyr Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Ala
                    85                  90                  95

ctt tat tta aga gtt gat cct tat tta gca tat caa tac cgt aat cat       336
Leu Tyr Leu Arg Val Asp Pro Tyr Leu Ala Tyr Gln Tyr Arg Asn His
                100                 105                 110

gat ggt gag gta ttg gaa aat gca gga cat gat tgg att ttc gat aaa       384
Asp Gly Glu Val Leu Glu Asn Ala Gly His Asp Trp Ile Phe Asp Lys
            115                 120                 125

atg aag cag ctt gga tat aaa cac caa gga ttt tta act ggt ttc gat       432
Met Lys Gln Leu Gly Tyr Lys His Gln Gly Phe Leu Thr Gly Phe Asp
        130                 135                 140

tca att att caa att agg ttc cac tct gta ctg gat tta gta ggt aaa       480
Ser Ile Ile Gln Ile Arg Phe His Ser Val Leu Asp Leu Val Gly Lys
145                 150                 155                 160

act gct aaa gat gta cta aat ggt atg gat agt tta cgt aaa cgt aat       528
Thr Ala Lys Asp Val Leu Asn Gly Met Asp Ser Leu Arg Lys Arg Asn
                165                 170                 175

act aaa aaa gta caa aaa aat ggc gtg aaa gta agg ttc tta agg gaa       576
Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Arg Glu
            180                 185                 190

gat gag ttg cca att ttc cgt tca ttc atg gaa gat aca tct gaa act       624
Asp Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr
            195                 200                 205

aaa gac ttt gac gat aga gac gat ggc ttt tac tac aat aga tta agg       672
Lys Asp Phe Asp Asp Arg Asp Asp Gly Phe Tyr Tyr Asn Arg Leu Arg
            210                 215                 220

tat tat aaa gat cgc gta tta gta cct cta gct tat atg gat ttc aat       720
Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Met Asp Phe Asn
225                 230                 235                 240

gaa tat att gaa gaa ttg caa gct gaa cgt gag gtg tta agc aaa gat       768
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18

```
Glu Tyr Ile Glu Glu Leu Gln Ala Glu Arg Glu Val Leu Ser Lys Asp
            245             250             255

atc aat aaa gca gta aaa gat atc gag aaa aga cct gaa aat aaa aaa    816
Ile Asn Lys Ala Val Lys Asp Ile Glu Lys Arg Pro Glu Asn Lys Lys
            260             265             270

gca tat aat aaa aaa gat aat cta gag aaa caa ctt ata gcg aat caa    864
Ala Tyr Asn Lys Lys Asp Asn Leu Glu Lys Gln Leu Ile Ala Asn Gln
            275             280             285

caa aaa att gat gaa gct aaa act cta caa gag aag cat ggt aac gaa    912
Gln Lys Ile Asp Glu Ala Lys Thr Leu Gln Glu Lys His Gly Asn Glu
            290             295             300

cta cca atc tca gca gca tat ttc atc att aac cct tat gaa gta gtg    960
Leu Pro Ile Ser Ala Ala Tyr Phe Ile Ile Asn Pro Tyr Glu Val Val
305             310             315             320

tat tat gcg ggt gga acg tca aat gag ttt aga cat ttt gct ggt agt   1008
Tyr Tyr Ala Gly Gly Thr Ser Asn Glu Phe Arg His Phe Ala Gly Ser
                325             330             335

tat gcc att caa tgg aag atg att aac tat gct att gac cat aat att   1056
Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Ile Asp His Asn Ile
            340             345             350

gat aga tat aat ttt tat gga att agt ggt cat ttt aca gaa gat gca   1104
Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly His Phe Thr Glu Asp Ala
            355             360             365

gaa gat gcc ggt gta gtt aaa ttt aaa aaa gga ttt aat gcg gat gta   1152
Glu Asp Ala Gly Val Val Lys Phe Lys Lys Gly Phe Asn Ala Asp Val
            370             375             380

gtg gaa tat gtt ggt gat ttt att aaa cca atc aat aaa cca atg tac   1200
Val Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr
385             390             395             400

aaa att tat acg aca tta aag aaa att aaa gat aaa aag aaa taa       1245
Lys Ile Tyr Thr Thr Leu Lys Lys Ile Lys Asp Lys Lys Lys
            405             410

acatttaata gaagggaact aagctagaat gaaatttaca gagttaaacc            1295


<210>  45
<211>  414
<212>  PRT
<213>  Staphylococcus xylosus femA

<400>  45

Thr Gln Lys Ser Leu Gly Ala Phe Ser Asp Lys Met Pro Asn Ser His
1               5               10              15
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19

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Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Ile Ala Glu Ser Thr
            20                  25              30

Glu Thr His Leu Val Gly Ile Lys Asn Asn Asp Asn Glu Val Ile Ala
            35                  40              45

Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
    50                  55              60

Tyr Thr Asn Arg Gly Pro Val Ile Asp Phe Glu Asn Lys Glu Leu Val
65                  70              75              80

His Tyr Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Ala
                85              90              95

Leu Tyr Leu Arg Val Asp Pro Tyr Leu Ala Tyr Gln Tyr Arg Asn His
            100             105             110

Asp Gly Glu Val Leu Glu Asn Ala Gly His Asp Trp Ile Phe Asp Lys
        115             120             125

Met Lys Gln Leu Gly Tyr Lys His Gln Gly Phe Leu Thr Gly Phe Asp
    130             135             140

Ser Ile Ile Gln Ile Arg Phe His Ser Val Leu Asp Leu Val Gly Lys
145             150             155             160

Thr Ala Lys Asp Val Leu Asn Gly Met Asp Ser Leu Arg Lys Arg Asn
            165             170             175

Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Arg Glu
            180             185             190

Asp Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr
        195             200             205

Lys Asp Phe Asp Asp Arg Asp Asp Gly Phe Tyr Tyr Asn Arg Leu Arg
    210             215             220

Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Met Asp Phe Asn
225             230             235             240

Glu Tyr Ile Glu Glu Leu Gln Ala Glu Arg Glu Val Leu Ser Lys Asp
```

Ile Asn Lys Ala Val Lys Asp Ile Glu Lys Arg Pro Glu Asn Lys Lys
          260   265   270

Ala Tyr Asn Lys Lys Asp Asn Leu Glu Lys Gln Leu Ile Ala Asn Gln
        275   280   285

Gln Lys Ile Asp Glu Ala Lys Thr Leu Gln Glu Lys His Gly Asn Glu
        290   295   300

Leu Pro Ile Ser Ala Ala Tyr Phe Ile Ile Asn Pro Tyr Glu Val Val
305   310   315   320

Tyr Tyr Ala Gly Gly Thr Ser Asn Glu Phe Arg His Phe Ala Gly Ser
          325   330   335

Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Ile Asp His Asn Ile
          340   345   350

Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly His Phe Thr Glu Asp Ala
        355   360   365

Glu Asp Ala Gly Val Val Lys Phe Lys Lys Gly Phe Asn Ala Asp Val
        370   375   380

Val Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr
385   390   395   400

Lys Ile Tyr Thr Thr Leu Lys Lys Ile Lys Asp Lys Lys Lys
          405   410

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<210>  46
<211>  1283
<212>  DNA
<213>  Staphylococcus capitis femA

<220>
<221>  CDS
<222>  (1)..(1236)

<400>  46
aca gct aaa gaa ttt agt gac ttt act gat caa atg cct tat agc cat      48
Thr Ala Lys Glu Phe Ser Asp Phe Thr Asp Gln Met Pro Tyr Ser His
1               5                   10                  15
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```
ttt act cag atg gaa ggt aat tat gaa ctt aaa gtt gct gaa ggt acg      96
Phe Thr Gln Met Glu Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Thr
        20              25              30

gat tca cat ctc gta gga att aaa aat aat gac aac caa gtg att gca     144
Asp Ser His Leu Val Gly Ile Lys Asn Asn Asp Asn Gln Val Ile Ala
        35              40              45

gca tgt tta tta act gct gta cct gta atg aaa att ttt aaa tat ttt     192
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Ile Phe Lys Tyr Phe
50              55              60

tac tca aat cgc ggg cca gtg att gat tat gat aat aaa gag ctt gtt     240
Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Asp Asn Lys Glu Leu Val
65              70              75              80

cac ttt ttc ttt aat gaa tta agt aaa tat gta aaa aag cat aat tgt     288
His Phe Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Cys
                85              90              95

ctt tat cta aga gtt gac cct tat ctt cct tat caa tac tta aat cat     336
Leu Tyr Leu Arg Val Asp Pro Tyr Leu Pro Tyr Gln Tyr Leu Asn His
            100             105             110

gac ggt gaa att att gga aat gct ggc cat gat tgg ttt ttc aat aag     384
Asp Gly Glu Ile Ile Gly Asn Ala Gly His Asp Trp Phe Phe Asn Lys
        115             120             125

atg gaa gaa tta gga ttt gaa cat gaa ggc ttt cat aaa ggc ttc cat     432
Met Glu Glu Leu Gly Phe Glu His Glu Gly Phe His Lys Gly Phe His
        130             135             140

cct atc tta caa gta aga tat cat tca gtt tta gat tta aaa gat aaa     480
Pro Ile Leu Gln Val Arg Tyr His Ser Val Leu Asp Leu Lys Asp Lys
145             150             155             160

acg gct aaa gat gta ctc aaa gga atg gat agt tta aga aag cgt aat     528
Thr Ala Lys Asp Val Leu Lys Gly Met Asp Ser Leu Arg Lys Arg Asn
            165             170             175

act aag aaa gta caa aaa aat ggt gtc aaa gtc cgt ttc cta tcc gaa     576
Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Glu
        180             185             190

gat gaa tta cct atc ttt aga tca ttt atg gaa gat act aca gaa acg     624
Asp Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Asp Thr Thr Glu Thr
        195             200             205

aaa gag ttc gcc gat aga gat gat agt ttc tat tat aat cga tta aaa     672
Lys Glu Phe Ala Asp Arg Asp Asp Ser Phe Tyr Tyr Asn Arg Leu Lys
        210             215             220

tac ttt aaa gat aga gta tta gta cca tta gca tat gtt gac ttc gat     720
Tyr Phe Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Val Asp Phe Asp
225             230             235             240

gag tat att gaa gaa ctt aat aat gaa aga gat gtt ctt aat aaa gat     768
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```
Glu Tyr Ile Glu Glu Leu Asn Asn Glu Arg Asp Val Leu Asn Lys Asp
            245                 250                 255

tta aat aag gcg ctc aaa gat att gag aag aga cct gat aat aag aaa     816
Leu Asn Lys Ala Leu Lys Asp Ile Glu Lys Arg Pro Asp Asn Lys Lys
            260                 265                 270

gct tat aac aaa aga gat aat ctt caa caa caa tta gat gca aat caa     864
Ala Tyr Asn Lys Arg Asp Asn Leu Gln Gln Gln Leu Asp Ala Asn Gln
            275                 280                 285

caa aaa att gat gaa gct aaa aac tta caa caa gaa cat ggt aat gaa     912
Gln Lys Ile Asp Glu Ala Lys Asn Leu Gln Gln Glu His Gly Asn Glu
            290                 295                 300

tta cct att tca gct gga tat ttc ttc att aat ccg ttt gaa gtt gtt     960
Leu Pro Ile Ser Ala Gly Tyr Phe Phe Ile Asn Pro Phe Glu Val Val
305                 310                 315                 320

tat tac gca ggt ggc aca tcg aat cgt tat cgt cac tat gcc gga agt    1008
Tyr Tyr Ala Gly Gly Thr Ser Asn Arg Tyr Arg His Tyr Ala Gly Ser
                    325                 330                 335

tat gca att caa tgg aaa atg ata aac tat gct tta gaa cat gga att    1056
Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Leu Glu His Gly Ile
            340                 345                 350

aac cgt tat aat ttt tat gga gtt agt ggg gac ttc agt gaa gac gct    1104
Asn Arg Tyr Asn Phe Tyr Gly Val Ser Gly Asp Phe Ser Glu Asp Ala
            355                 360                 365

gaa gat gta gga gta att aag ttc aaa aaa ggc tat aat gct gat gtt    1152
Glu Asp Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val
            370                 375                 380

att gaa tat gta ggt gat ttt atc aag cca atc aat aaa cct atg tat    1200
Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr
385                 390                 395                 400

gca atc tat aac gca ctt aaa aag tta aag aaa tag attttttac          1246
Ala Ile Tyr Asn Ala Leu Lys Lys Leu Lys Lys
            405                 410

caacccaatt atctaattat gaaatttaca gagttaa                           1283


<210>   47
<211>   411
<212>   PRT
<213>   Staphylococcus capitis femA

<400>   47

Thr Ala Lys Glu Phe Ser Asp Phe Thr Asp Gln Met Pro Tyr Ser His
1               5                   10                  15
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23

Phe Thr Gln Met Glu Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Thr
          20   25   30

Asp Ser His Leu Val Gly Ile Lys Asn Asn Asp Asn Gln Val Ile Ala
          35   40   45

Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Ile Phe Lys Tyr Phe
50   55   60

Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Asp Asn Lys Glu Leu Val
65   70   75   80

His Phe Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Cys
                  85   90   95

Leu Tyr Leu Arg Val Asp Pro Tyr Leu Pro Tyr Gln Tyr Leu Asn His
              100   105   110

Asp Gly Glu Ile Ile Gly Asn Ala Gly His Asp Trp Phe Phe Asn Lys
          115   120   125

Met Glu Glu Leu Gly Phe Glu His Glu Gly Phe His Lys Gly Phe His
      130   135   140

Pro Ile Leu Gln Val Arg Tyr His Ser Val Leu Asp Leu Lys Asp Lys
145   150   155   160

Thr Ala Lys Asp Val Leu Lys Gly Met Asp Ser Leu Arg Lys Arg Asn
              165   170   175

Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Glu
          180   185   190

Asp Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Asp Thr Thr Glu Thr
          195   200   205

Lys Glu Phe Ala Asp Arg Asp Asp Ser Phe Tyr Tyr Asn Arg Leu Lys
      210   215   220

Tyr Phe Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Val Asp Phe Asp
225   230   235   240

Glu Tyr Ile Glu Glu Leu Asn Asn Glu Arg Asp Val Leu Asn Lys Asp

```
Leu Asn Lys Ala Leu Lys Asp Ile Glu Lys Arg Pro Asp Asn Lys Lys
            260             265             270

Ala Tyr Asn Lys Arg Asp Asn Leu Gln Gln Gln Leu Asp Ala Asn Gln
        275             280             285

Gln Lys Ile Asp Glu Ala Lys Asn Leu Gln Gln Glu His Gly Asn Glu
    290             295             300

Leu Pro Ile Ser Ala Gly Tyr Phe Phe Ile Asn Pro Phe Glu Val Val
305             310             315             320

Tyr Tyr Ala Gly Gly Thr Ser Asn Arg Tyr Arg His Tyr Ala Gly Ser
            325             330             335

Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Leu Glu His Gly Ile
        340             345             350

Asn Arg Tyr Asn Phe Tyr Gly Val Ser Gly Asp Phe Ser Glu Asp Ala
        355             360             365

Glu Asp Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val
    370             375             380

Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr
385             390             395             400

Ala Ile Tyr Asn Ala Leu Lys Lys Leu Lys Lys
            405             410
```

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<210>  48
<211>  1297
<212>  DNA
<213>  Staphylococcus schleiferi femA

<220>
<221>  CDS
<222>  (1)..(1248)

<400>  48
acg acg gct gaa ttt ggt gcg ttt aca gat caa atg cca tat agc cat      48
Thr Thr Ala Glu Phe Gly Ala Phe Thr Asp Gln Met Pro Tyr Ser His
1               5                   10                  15
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```
ttc acg caa atg gta ggg aac tat gaa tta aag gtt gct gaa ggt gtt        96
Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Val
         20                  25                  30

gaa aca cat ctt gtc ggc att aaa gat aac aac aat aac gta cta gca       144
Glu Thr His Leu Val Gly Ile Lys Asp Asn Asn Asn Asn Val Leu Ala
         35                  40                  45

gca tgt tta ctg aca gca gtg cca gta atg aag ttt ttt aaa tat ttt      192
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
 50                  55                  60

tat tca aac cgc gga cca gtc atg gac tac gaa aat aaa gag ctc gtt      240
Tyr Ser Asn Arg Gly Pro Val Met Asp Tyr Glu Asn Lys Glu Leu Val
65                  70                  75                  80

cat ttc ttt ttt aat gaa ctt tca aaa tat gtt aag aaa tat cac gca      288
His Phe Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys Tyr His Ala
                     85                  90                  95

ttg tat ttg aga gta gac cct tat tta cca atg tta aag cga aac cat      336
Leu Tyr Leu Arg Val Asp Pro Tyr Leu Pro Met Leu Lys Arg Asn His
             100                 105                 110

gat ggt gaa gtg att gaa aga tac ggc agt gac tgg ttt ttt gat aaa      384
Asp Gly Glu Val Ile Glu Arg Tyr Gly Ser Asp Trp Phe Phe Asp Lys
         115                 120                 125

atg gct gaa tta aac ttt gaa cat gaa ggt ttc aca act ggg ttt gat      432
Met Ala Glu Leu Asn Phe Glu His Glu Gly Phe Thr Thr Gly Phe Asp
     130                 135                 140

aca ata agg caa att cgt ttt cat tct gtg ctc gat gtt gaa aat aaa      480
Thr Ile Arg Gln Ile Arg Phe His Ser Val Leu Asp Val Glu Asn Lys
145                 150                 155                 160

aca tca aaa gac atc tta aat caa atg gat aat tta agg aaa aga aat      528
Thr Ser Lys Asp Ile Leu Asn Gln Met Asp Asn Leu Arg Lys Arg Asn
                 165                 170                 175

acg aaa aaa gta cag aaa aat ggt gtg aaa gtc cgc tat cta aac gaa      576
Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Tyr Leu Asn Glu
             180                 185                 190

gat gaa tta cat att ttc cgt tcg ttt atg gaa gat aca tct gaa aca      624
Asp Glu Leu His Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr
         195                 200                 205

aaa gat ttt gta gat aga gat gac gat ttt tat tat cat cgt atg aaa      672
Lys Asp Phe Val Asp Arg Asp Asp Asp Phe Tyr Tyr His Arg Met Lys
     210                 215                 220

tac tat aaa gat cgt gtc cgc gta cca cta gcg tat att gat ttt aat      720
Tyr Tyr Lys Asp Arg Val Arg Val Pro Leu Ala Tyr Ile Asp Phe Asn
225                 230                 235                 240

gca tat tta gca gag ctc aac act gaa gcg caa gac ttt aaa aaa gaa      768
```

26

```
Ala Tyr Leu Ala Glu Leu Asn Thr Glu Ala Gln Asp Phe Lys Lys Glu
            245                 250                 255

att gca aaa gca gat aaa gac atc gac aag cgt cct gaa aat cag aaa      816
Ile Ala Lys Ala Asp Lys Asp Ile Asp Lys Arg Pro Glu Asn Gln Lys
            260                 265                 270

gcc ata aat aaa aag aaa aat tta gag caa caa cta gaa gcg aat caa      864
Ala Ile Asn Lys Lys Lys Asn Leu Glu Gln Gln Leu Glu Ala Asn Gln
            275                 280                 285

gct aaa ata aaa gaa gca gaa aca ttg caa ctt aaa cac ggt gac aca      912
Ala Lys Ile Lys Glu Ala Glu Thr Leu Gln Leu Lys His Gly Asp Thr
        290                 295                 300

tta ccg att tcg gct gga ttc ttt att att aat cca ttt gag gtt gtt      960
Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val
305                 310                 315                 320

tat tat gca ggc ggc aca gca aac gaa ttt cgt cat ttt gct gga agc     1008
Tyr Tyr Ala Gly Gly Thr Ala Asn Glu Phe Arg His Phe Ala Gly Ser
                325                 330                 335

tac gca gtg caa tgg gaa atg att aat tat gcg att gat tat caa att     1056
Tyr Ala Val Gln Trp Glu Met Ile Asn Tyr Ala Ile Asp Tyr Gln Ile
                340                 345                 350

cca aga tat aac ttt tat ggc att agt ggt gat ttt tca gaa gat gca     1104
Pro Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala
            355                 360                 365

gaa gat gca ggt gtg ata aaa ttt aaa aaa ggc tat aat gca gaa gta     1152
Glu Asp Ala Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Glu Val
        370                 375                 380

ata gaa tat gtc ggt gat ttt att aag cct ata aac aaa cct gcc tat     1200
Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Ala Tyr
385                 390                 395                 400

aca gtc tac tta aaa tta aag caa tta aaa gac aag ata aaa aga taa     1248
Thr Val Tyr Leu Lys Leu Lys Gln Leu Lys Asp Lys Ile Lys Arg
            405                 410                 415

gatatagcaa agagaagggg atttattggt atgaaattta cagagttaa              1297


<210>   49
<211>   415
<212>   PRT
<213>   Staphylococcus schleiferi femA

<400>   49

Thr Thr Ala Glu Phe Gly Ala Phe Thr Asp Gln Met Pro Tyr Ser His
1               5                   10                  15
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27

Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Val
          20   25   30

Glu Thr His Leu Val Gly Ile Lys Asp Asn Asn Asn Asn Val Leu Ala
          35   40   45

Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
    50   55   60

Tyr Ser Asn Arg Gly Pro Val Met Asp Tyr Glu Asn Lys Glu Leu Val
65   70   75.   80

His Phe Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys Tyr His Ala
                  85   90   95

Leu Tyr Leu Arg Val Asp Pro Tyr Leu Pro Met Leu Lys Arg Asn His
              100   105   110

Asp Gly Glu Val Ile Glu Arg Tyr Gly Ser Asp Trp Phe Phe Asp Lys
          115   120   125

Met Ala Glu Leu Asn Phe Glu His Glu Gly Phe Thr Thr Gly Phe Asp
    130   135   140

Thr Ile Arg Gln Ile Arg Phe His Ser Val Leu Asp Val Glu Asn Lys
145   150   155   160

Thr Ser Lys Asp Ile Leu Asn Gln Met Asp Asn Leu Arg Lys Arg Asn
              165   170   175

Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Tyr Leu Asn Glu
              180   185   190

Asp Glu Leu His Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr
          195   200   205

Lys Asp Phe Val Asp Arg Asp Asp Phe Tyr Tyr His Arg Met Lys
    210   215   220

Tyr Tyr Lys Asp Arg Val Arg Val Pro Leu Ala Tyr Ile Asp Phe Asn
225   230   235   240

Ala Tyr Leu Ala Glu Leu Asn Thr Glu Ala Gln Asp Phe Lys Lys Glu

28

Ile Ala Lys Ala Asp Lys Asp Ile Asp Lys Arg Pro Glu Asn Gln Lys
            260   265   270

Ala Ile Asn Lys Lys Lys Asn Leu Glu Gln Gln Leu Glu Ala Asn Gln
        275   280   285

Ala Lys Ile Lys Glu Ala Glu Thr Leu Gln Leu Lys His Gly Asp Thr
    290   295   300

Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val
305   310   315   320

Tyr Tyr Ala Gly Gly Thr Ala Asn Glu Phe Arg His Phe Ala Gly Ser
                325   330   335

Tyr Ala Val Gln Trp Glu Met Ile Asn Tyr Ala Ile Asp Tyr Gln Ile
            340   345   350

Pro Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala
        355   360   365

Glu Asp Ala Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Glu Val
    370   375   380

Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Ala Tyr
385   390   395   400

Thr Val Tyr Leu Lys Leu Lys Gln Leu Lys Asp Lys Ile Lys Arg
                405   410   415

<210>   50
<211>   1284
<212>   DNA
<213>   Staphylococcus sciuri femA

<220>
<221>   CDS
<222>   (1)..(1233)

<400>   50
aca ctg gaa ttt gaa gct ttt aca aat aaa atg ccg tac gcg cat ttt   48
Thr Leu Glu Phe Glu Ala Phe Thr Asn Lys Met Pro Tyr Ala His Phe
1   5   10   15

29

```
aca caa gca gta ggt aat tat gaa tta aaa aca tct gaa ggt act tca      96
Thr Gln Ala Val Gly Asn Tyr Glu Leu Lys Thr Ser Glu Gly Thr Ser
         20              25              30

aca cat tta gta ggg gtc aaa gat aat caa ggt gaa gta tta gct gcg     144
Thr His Leu Val Gly Val Lys Asp Asn Gln Gly Glu Val Leu Ala Ala
         35              40              45

tgt ctg tta aca agt gta cca gtt atg aag aaa ttt aat tac ttt tac     192
Cys Leu Leu Thr Ser Val Pro Val Met Lys Lys Phe Asn Tyr Phe Tyr
         50              55              60

tca aat aga gga cca gta atg gat tat gac aac aaa gaa ctt gtt gac     240
Ser Asn Arg Gly Pro Val Met Asp Tyr Asp Asn Lys Glu Leu Val Asp
65               70              75              80

ttt ttc ttt aaa gaa atc gtg agc tat tta aaa agt tat aaa gga tta     288
Phe Phe Phe Lys Glu Ile Val Ser Tyr Leu Lys Ser Tyr Lys Gly Leu
             85              90              95

ttc ttt aga atc gat cct tac ttg cca tat caa cta aga gat cat gat     336
Phe Phe Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Leu Arg Asp His Asp
             100             105             110

ggc aat att aaa aaa tca ttc aac cgt gat ggt tta att aaa caa ttt     384
Gly Asn Ile Lys Lys Ser Phe Asn Arg Asp Gly Leu Ile Lys Gln Phe
         115             120             125

gaa tca tta ggt tat gaa cac caa ggc ttc aca act ggt ttc cac cca     432
Glu Ser Leu Gly Tyr Glu His Gln Gly Phe Thr Thr Gly Phe His Pro
         130             135             140

ata cat caa att aga tgg cat tct gta ctt gat tta gaa agt atg gac     480
Ile His Gln Ile Arg Trp His Ser Val Leu Asp Leu Glu Ser Met Asp
145             150             155             160

gaa aag acg ctc atc aag aac atg gac agt tta aga aaa aga aat act     528
Glu Lys Thr Leu Ile Lys Asn Met Asp Ser Leu Arg Lys Arg Asn Thr
                 165             170             175

aaa aaa gtt caa aaa aat ggt gtt aaa gtt cgt ttt cta tct aaa gat     576
Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Lys Asp
         180             185             190

gaa atg ccg ata ttc cgt caa ttt atg gaa gat act aca gag aag aaa     624
Glu Met Pro Ile Phe Arg Gln Phe Met Glu Asp Thr Thr Glu Lys Lys
         195             200             205

gat ttc aac gat cgt ggc gat gac ttc tat tac aat aga tta aaa tac     672
Asp Phe Asn Asp Arg Gly Asp Asp Phe Tyr Tyr Asn Arg Leu Lys Tyr
         210             215             220

ttt gaa aat gta aag att cct tta gca tat ata gac ttt gaa act tac     720
Phe Glu Asn Val Lys Ile Pro Leu Ala Tyr Ile Asp Phe Glu Thr Tyr
225             230             235             240

att cca caa tta gaa aaa gaa cat gaa caa tac aac aaa gat att gca     768
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30

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Ile Pro Gln Leu Glu Lys Glu His Glu Gln Tyr Asn Lys Asp Ile Ala
                245                 250                 255

aaa gct gaa aaa gat tta gaa aag aaa'cca gat aat caa aaa acg att       816
Lys Ala Glu Lys Asp Leu Glu Lys Lys Pro Asp Asn Gln Lys Thr Ile
                260                 265                 270

aat aaa ata gac aac tta aaa caa caa aga gaa gca aat gaa gct aaa       864
Asn Lys Ile Asp Asn Leu Lys Gln Gln Arg Glu Ala Asn Glu Ala Lys
                275                 280                 285

tta gaa gaa gca ctt caa cta caa caa gaa cat ggt gat aca tta cca       912
Leu Glu Glu Ala Leu Gln Leu Gln Gln Glu His Gly Asp Thr Leu Pro
                290                 295                 300

ata gca gct ggt ttc ttt att att aat cca ttt gaa gtt gta tat tat      960
Ile Ala Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val Tyr Tyr
305                 310                 315                 320

gca ggt ggt tca tcg aat gaa tat cgt cac ttt gca ggt agt tat gca      1008
Ala Gly Gly Ser Ser Asn Glu Tyr Arg His Phe Ala Gly Ser Tyr Ala
                    325                 330                 335

att cag tgg gaa atg att aaa tac gcg tta gat cac aac att gac cgt      1056
Ile Gln Trp Glu Met Ile Lys Tyr Ala Leu Asp His Asn Ile Asp Arg
                340                 345                 350

tat aac ttc tat ggt atc agc gga gac ttc tca gaa gat gca cct gat      1104
Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala Pro Asp
                355                 360                 365

gtt ggc gtt att aaa ttt aaa aaa ggt tac aat gca gat gtt tat gaa      1152
Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val Tyr Glu
                370                 375                 380

tat att ggt gat ttc gtt aaa cca att aat aaa cca gcg tac aaa gca      1200
Tyr Ile Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Ala Tyr Lys Ala
385                 390                 395                 400

tat aca aca cta aaa aaa gta tta aaa aaa taa atgattttca gtaagagagg    1253
Tyr Thr Thr Leu Lys Lys Val Leu Lys Lys
                405                 410

                                                                      1284
aatttagata atatgaaatt tacagagtta a
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<210> 51
<211> 410
<212> PRT
<213> Staphylococcus sciuri femA

<400> 51

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Thr Leu Glu Phe Glu Ala Phe Thr Asn Lys Met Pro Tyr Ala His Phe
1               5                   10                  15
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Thr Gln Ala Val Gly Asn Tyr Glu Leu Lys Thr Ser Glu Gly Thr Ser
            20   25   30

Thr His Leu Val Gly Val Lys Asp Asn Gln Gly Glu Val Leu Ala Ala
        35   40   45

Cys Leu Leu Thr Ser Val Pro Val Met Lys Lys Phe Asn Tyr Phe Tyr
    50   55   60

Ser Asn Arg Gly Pro Val Met Asp Tyr Asp Asn Lys Glu Leu Val Asp
65   70   75   80

Phe Phe Phe Lys Glu Ile Val Ser Tyr Leu Lys Ser Tyr Lys Gly Leu
            85   90   95

Phe Phe Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Leu Arg Asp His Asp
            100   105   110

Gly Asn Ile Lys Lys Ser Phe Asn Arg Asp Gly Leu Ile Lys Gln Phe
        115   120   125

Glu Ser Leu Gly Tyr Glu His Gln Gly Phe Thr Thr Gly Phe His Pro
    130   135   140

Ile His Gln Ile Arg Trp His Ser Val Leu Asp Leu Glu Ser Met Asp
145   150   155   160

Glu Lys Thr Leu Ile Lys Asn Met Asp Ser Leu Arg Lys Arg Asn Thr
            165   170   175

Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Lys Asp
        180   185   190

Glu Met Pro Ile Phe Arg Gln Phe Met Glu Asp Thr Thr Glu Lys Lys
        195   200   205

Asp Phe Asn Asp Arg Gly Asp Asp Phe Tyr Tyr Asn Arg Leu Lys Tyr
    210   215   220

Phe Glu Asn Val Lys Ile Pro Leu Ala Tyr Ile Asp Phe Glu Thr Tyr
225   230   235   240

Ile Pro Gln Leu Glu Lys Glu His Glu Gln Tyr Asn Lys Asp Ile Ala

Lys Ala Glu Lys Asp Leu Glu Lys Lys Pro Asp Asn Gln Lys Thr Ile
            260   265   270

Asn Lys Ile Asp Asn Leu Lys Gln Gln Arg Glu Ala Asn Glu Ala Lys
        275   280   285

Leu Glu Glu Ala Leu Gln Leu Gln Gln Glu His Gly Asp Thr Leu Pro
    290   295   300

Ile Ala Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val Tyr Tyr
305   310   315   320

Ala Gly Gly Ser Ser Asn Glu Tyr Arg His Phe Ala Gly Ser Tyr Ala
            325   330   335

Ile Gln Trp Glu Met Ile Lys Tyr Ala Leu Asp His Asn Ile Asp Arg
            340   345   350

Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala Pro Asp
        355   360   365

Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val Tyr Glu
    370   375   380

Tyr Ile Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Ala Tyr Lys Ala
385   390   395   400

Tyr Thr Thr Leu Lys Lys Val Leu Lys Lys
                405   410

<210>   52
<211>   1343
<212>   DNA
<213>   Staphylococcus hominis femA

<220>
<221>   CDS
<222>   (64)..(1317)

<400>   52
taaaatttta aaattagtca actcaaatta aataaagatt ctaaattagg agttatagag   60

ata atg aag ttt aca aat tta aca gct aca gaa ttt ggc gat ttt act   108
    Met Lys Phe Thr Asn Leu Thr Ala Thr Glu Phe Gly Asp Phe Thr

33

```
gaa aaa atg cca tat agc cat ttt aca cag atg act gaa aat tat gag      156
Glu Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu
            20              25              30

tta aaa gtt gct gag aaa act gaa act cat tta gta gga att aaa aat      204
Leu Lys Val Ala Glu Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn
        35              40              45

aaa gat aat gaa gtc att gct gct tgt atg cta act gct gta ccc gtt      252
Lys Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val
        50              55              60

atg aaa att ttt aaa tat ttt tat tca aat cgt ggt cca gtc att gat      300
Met Lys Ile Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp
    65              70              75

tat gaa aac aaa gaa ctc gtt cac ttt ttc ttt aac gaa tta agt aaa      348
Tyr Glu Asn Lys Glu Leu Val His Phe Phe Phe Asn Glu Leu Ser Lys
80              85              90              95

tat tta aaa caa caa cat tgt tta tat gta cgt ata gac cct tat ttg      396
Tyr Leu Lys Gln Gln His Cys Leu Tyr Val Arg Ile Asp Pro Tyr Leu
            100             105             110

cct tat caa tat cgt aat cat gat ggt gat att aca gga aat gct ggg      444
Pro Tyr Gln Tyr Arg Asn His Asp Gly Asp Ile Thr Gly Asn Ala Gly
            115             120             125

aat gat tgg ttc ttc gat aaa atg aaa caa tta gga tat caa cac gaa      492
Asn Asp Trp Phe Phe Asp Lys Met Lys Gln Leu Gly Tyr Gln His Glu
            130             135             140

ggg ttt aca aca gga ttt gat cca ata tta caa att cgg ttc cat tca      540
Gly Phe Thr Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser
    145             150             155

gtt tta aat tta aag gat aaa act gct aaa gat gta tta aat gga atg      588
Val Leu Asn Leu Lys Asp Lys Thr Ala Lys Asp Val Leu Asn Gly Met
160             165             170             175

gat agt tta cga aaa aga aat act aaa aaa gtc caa aaa aat ggt gtt      636
Asp Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val
            180             185             190

aaa gta aga ttt ctt act aaa gaa gaa tta cct att ttc aga tca ttt      684
Lys Val Arg Phe Leu Thr Lys Glu Glu Leu Pro Ile Phe Arg Ser Phe
            195             200             205

atg gaa gat aca tca gag act aaa gaa ttt tct gat aga gag gat agt      732
Met Glu Asp Thr Ser Glu Thr Lys Glu Phe Ser Asp Arg Glu Asp Ser
            210             215             220

ttt tac tat aat cga ttt gat cat ttt aaa gat aga gta tta gta cct      780
Phe Tyr Tyr Asn Arg Phe Asp His Phe Lys Asp Arg Val Leu Val Pro
    225             230             235
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ctc gca tat ata aaa ttt gat gaa tat ctt gaa gaa ctt cat gca gaa      828
Leu Ala Tyr Ile Lys Phe Asp Glu Tyr Leu Glu Glu Leu His Ala Glu
240             245             250                 255

cgt cag aca tta aat aaa gac tta aac aaa gct cta aaa gat att gaa      876
Arg Gln Thr Leu Asn Lys Asp Leu Asn Lys Ala Leu Lys Asp Ile Glu
                260             265                 270

aaa cga cca gat aac aaa aaa gca caa aat aaa aaa ata aat tta gaa      924
Lys Arg Pro Asp Asn Lys Lys Ala Gln Asn Lys Lys Ile Asn Leu Glu
                275             280                 285

cag caa tta aaa gca aat gag caa aaa att gat gaa gca aca caa ctt      972
Gln Gln Leu Lys Ala Asn Glu Gln Lys Ile Asp Glu Ala Thr Gln Leu
                290             295                 300

caa tta gaa cat ggt aac gaa tta cca ata tct gct gga ttc ttc ttt     1020
Gln Leu Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe
                305             310             315

att aat cca ttt gaa gtt gta tat tat gca ggt gga acg tca aat aaa     1068
Ile Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys
320             325             330                 335

tat aga cac ttc gct gga agt tat gca gtt caa tgg act atg att aat     1116
Tyr Arg His Phe Ala Gly Ser Tyr Ala Val Gln Trp Thr Met Ile Asn
                340             345             350

tat ·gca att gat cat ggc att gac cgt tat aat ttt tat ggg att agt    1164
Tyr Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser
                355             360             365

ggt cat ttt aca gat gat gct gaa gat gca ggt gtt gta aaa ttt aaa     1212
Gly His Phe Thr Asp Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys
                370             375             380

aaa gga ttt aat gca gat gta att gaa tat gtt ggt gat ttc gtt aaa     1260
Lys Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys
385             390             395

cct ata aat aaa cca atg tat tca cta tat aca aca ctt aaa aaa att     1308
Pro Ile Asn Lys Pro Met Tyr Ser Leu Tyr Thr Thr Leu Lys Lys Ile
400             405             410                 415

aaa aag aga ttgaattaag aggggaatag tgagaa                            1343
Lys Lys Arg
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<210> 53
<211> 418
<212> PRT
<213> Staphylococcus hominis.femA

<400> 53

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Met Lys Phe Thr Asn Leu Thr Ala Thr Glu Phe Gly Asp Phe Thr Glu
1               5                   10                  15

Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu Leu
                20              25                  30

Lys Val Ala Glu Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn Lys
        35              40                  45

Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val Met
        50              55                  60

Lys Ile Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr
65              70                  75                  80

Glu Asn Lys Glu Leu Val His Phe Phe Phe Asn Glu Leu Ser Lys Tyr
                85                  90                  95

Leu Lys Gln Gln His Cys Leu Tyr Val Arg Ile Asp Pro Tyr Leu Pro
            100                 105                 110

Tyr Gln Tyr Arg Asn His Asp Gly Asp Ile Thr Gly Asn Ala Gly Asn
            115                 120                 125

Asp Trp Phe Phe Asp Lys Met Lys Gln Leu Gly Tyr Gln His Glu Gly
            130                 135                 140

Phe Thr Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser Val
145                 150                 155                 160

Leu Asn Leu Lys Asp Lys Thr Ala Lys Asp Val Leu Asn Gly Met Asp
                165                 170                 175

Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val Lys
                180                 185                 190

Val Arg Phe Leu Thr Lys Glu Glu Leu Pro Ile Phe Arg Ser Phe Met
            195                 200                 205

Glu Asp Thr Ser Glu Thr Lys Glu Phe Ser Asp Arg Glu Asp Ser Phe
            210                 215                 220

Tyr Tyr Asn Arg Phe Asp His Phe Lys Asp Arg Val Leu Val Pro Leu
```

36

Ala Tyr Ile Lys Phe Asp Glu Tyr Leu Glu Glu Leu His Ala Glu Arg
                245   250   255

Gln Thr Leu Asn Lys Asp Leu Asn Lys Ala Leu Lys Asp Ile Glu Lys
                260   265   270

Arg Pro Asp Asn Lys Lys Ala Gln Asn Lys Lys Ile Asn Leu Glu Gln
                275   280   285

Gln Leu Lys Ala Asn Glu Gln Lys Ile Asp Glu Ala Thr Gln Leu Gln
                290   295   300

Leu Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe Ile
305   310   315   320

Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys Tyr
                325   330   335

Arg His Phe Ala Gly Ser Tyr Ala Val Gln Trp Thr Met Ile Asn Tyr
                340   345   350

Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly
                355   360   365

His Phe Thr Asp Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys Lys
370   375   380

Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys Pro
385   390   395   400

Ile Asn Lys Pro Met Tyr Ser Leu Tyr Thr Thr Leu Lys Lys Ile Lys
                405   410   415

Lys Arg

<210> 54
<211> 1371
<212> DNA
<213> Staphylococcus saprophyticus femA

<220>

37

<221> CDS
<222> (64)..(1326)

<400> 54
acttgtttag attagaatta aactcgaaaa tagaactata gataaatagg agtatataaa   60

aaa atg aaa ttt acg aat tta act gca aaa gag ttc ggt gca ttt acg   108
    Met Lys Phe Thr Asn Leu Thr Ala Lys Glu Phe Gly Ala Phe Thr
    1   5   10   15

gat aaa atg ccg aat agt cat ttt acg caa atg gtt gga aat tat gaa   156
Asp Lys Met Pro Asn Ser His Phe Thr Gln Met Val Gly Asn Tyr Glu
          20   25   30

ttg aaa att gca gaa agt aca gaa aca cac cta gta ggt att aag aat   204
Leu Lys Ile Ala Glu Ser Thr Glu Thr His Leu Val Gly Ile Lys Asn
          35   40   45

aat gat aat gaa gta att gca gca tgt tta ctt aca gct gtt cct gtt   252
Asn Asp Asn Glu Val Ile Ala Ala Cys Leu Leu Thr Ala Val Pro Val
          50   55   60

atg aaa ttc ttc aag tat ttt tat tcc aat aga ggt cca gtc ata gat   300
Met Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp
          65   70   75

ttt gaa aat aaa gaa ctc gta cat tac ttc ttt aac gaa tta gca aaa   348
Phe Glu Asn Lys Glu Leu Val His Tyr Phe Phe Asn Glu Leu Ala Lys
80   85   90   95

tat gta aaa aaa cat aat gcc tta tat tta cga gta gat cct tat ctt   396
Tyr Val Lys Lys His Asn Ala Leu Tyr Leu Arg Val Asp Pro Tyr Leu
          100   105   110

gct tat caa tat cgt aat cat gat ggt gaa gta tta gca aat gcg ggt   444
Ala Tyr Gln Tyr Arg Asn His Asp Gly Glu Val Leu Ala Asn Ala Gly
          115   120   125

cac gat tgg att ttt gat aaa atg aaa caa ctc ggt tat aag cat gaa   492
His Asp Trp Ile Phe Asp Lys Met Lys Gln Leu Gly Tyr Lys His Glu
          130   135   140

ggt ttt tta act ggc ttt gac cca ata ctt caa ata aga ttc cat tct   540
Gly Phe Leu Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser
          145   150   155

gtt tta gat tta gct gga aaa act gct aaa gac gta ctt aat ggt atg   588
Val Leu Asp Leu Ala Gly Lys Thr Ala Lys Asp Val Leu Asn Gly Met
160   165   170   175

gat agt tta cgt aaa cga aat act aaa aaa gta cag aaa aat ggt gtg   636
Asp Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val
          180   185   190

aaa gta aga ttt tta ggt gaa gat gag ttg cca ata ttc cgc tca ttc   684
Lys Val Arg Phe Leu Gly Glu Asp Glu Leu Pro Ile Phe Arg Ser Phe
          195   200   205

38

atg gaa gat act tct gaa aca aag gat ttt gac gat aga gat gac gat   732
Met Glu Asp Thr Ser Glu Thr Lys Asp Phe Asp Asp Arg Asp Asp Asp
        210   215   220

ttt tat tat aat agg tta aga tat tat aaa gat cgt gtg ctt gtc cca   780
Phe Tyr Tyr Asn Arg Leu Arg Tyr Tyr Lys Asp Arg Val Leu Val Pro
        225   230   235

tta gct tat atg gat ttt gat gaa tat ata aca gaa tta aag gct gaa   828
Leu Ala Tyr Met Asp Phe Asp Glu Tyr Ile Thr Glu Leu Lys Ala Glu
240   245   250   255

cgc gaa gta tta agt aaa gat ata aat aaa gca gtt aag gat ata gaa   876
Arg Glu Val Leu Ser Lys Asp Ile Asn Lys Ala Val Lys Asp Ile Glu
                260   265   270

aaa aga cca gaa aat aaa aaa gcg tat aat aaa aaa gaa aat tta gaa   924
Lys Arg Pro Glu Asn Lys Lys Ala Tyr Asn Lys Lys Glu Asn Leu Glu
                275   280   285

caa caa ctg att gca aac caa caa aaa ata gat gaa gcc act gcg tta   972
Gln Gln Leu Ile Ala Asn Gln Gln Lys Ile Asp Glu Ala Thr Ala Leu
        290   295   300

caa gag aag cat ggt aac gaa tta ccg att tct gca gct tac ttt att   1020
Gln Glu Lys His Gly Asn Glu Leu Pro Ile Ser Ala Ala Tyr Phe Ile
        305   310   315

att aat cct tat gaa gtc gtt tac tat gca ggt ggt aca tct aat gaa   1068
Ile Asn Pro Tyr Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Glu
320   325   330   335

ttt aga cat ttt gct ggt agt tat gca ata caa tgg aag atg att aat   1116
Phe Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Lys Met Ile Asn
                340   345   350

tat gct ata gat cat aat ata gat aga tat aat ttt tat ggt att agt   1164
Tyr Ala Ile Asp His Asn Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser
                355   360   365

ggt cat ttt act gaa gat gca gaa gat gca ggt gtt gtt aaa ttt aaa   1212
Gly His Phe Thr Glu Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys
        370   375   380

aaa ggt ttt aat gca gat gta gta gaa tat gtt ggt gat ttt att aaa   1260
Lys Gly Phe Asn Ala Asp Val Val Glu Tyr Val Gly Asp Phe Ile Lys
        385   390   395

ccg att aat aag cca atg tac aaa att tat acg aca ttg aaa aaa att   1308
Pro Ile Asn Lys Pro Met Tyr Lys Ile Tyr Thr Thr Leu Lys Lys Ile
400   405   410   415

aag gat aaa aag aaa taa acataaatag aagggaacta agctagaatg   1356
Lys Asp Lys Lys Lys
        420

aaatttacag agtta

<210> 55
<211> 420
<212> PRT
<213> Staphylococcus saprophyticus femA

<400> 55

Met Lys Phe Thr Asn Leu Thr Ala Lys Glu Phe Gly Ala Phe Thr Asp
1   5   10   15

Lys Met Pro Asn Ser His Phe Thr Gln Met Val Gly Asn Tyr Glu Leu
                20   25   30

Lys Ile Ala Glu Ser Thr Glu Thr His Leu Val Gly Ile Lys Asn Asn
            35   40   45

Asp Asn Glu Val Ile Ala Ala Cys Leu Leu Thr Ala Val Pro Val Met
        50   55   60

Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp Phe
65   70   75   80

Glu Asn Lys Glu Leu Val His Tyr Phe Phe Asn Glu Leu Ala Lys Tyr
                85   90   95

Val Lys Lys His Asn Ala Leu Tyr Leu Arg Val Asp Pro Tyr Leu Ala
                100   105   110

Tyr Gln Tyr Arg Asn His Asp Gly Glu Val Leu Ala Asn Ala Gly His
            115   120   125

Asp Trp Ile Phe Asp Lys Met Lys Gln Leu Gly Tyr Lys His Glu Gly
        130   135   140

Phe Leu Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser Val
145   150   155   160

Leu Asp Leu Ala Gly Lys Thr Ala Lys Asp Val Leu Asn Gly Met Asp
                165   170   175

Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val Lys
            180   185   190

40

Val Arg Phe Leu Gly Glu Asp Glu Leu Pro Ile Phe Arg Ser Phe Met
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Glu Asp Thr Ser Glu Thr Lys Asp Phe Asp Asp Arg Asp Asp Asp Phe
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Tyr Tyr Asn Arg Leu Arg Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu
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Ala Tyr Met Asp Phe Asp Glu Tyr Ile Thr Glu Leu Lys Ala Glu Arg
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Glu Val Leu Ser Lys Asp Ile Asn Lys Ala Val Lys Asp Ile Glu Lys
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Arg Pro Glu Asn Lys Lys Ala Tyr Asn Lys Lys Glu Asn Leu Glu Gln
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Gln Leu Ile Ala Asn Gln Gln Lys Ile Asp Glu Ala Thr Ala Leu Gln
        290   295   300

Glu Lys His Gly Asn Glu Leu Pro Ile Ser Ala Ala Tyr Phe Ile Ile
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Asn Pro Tyr Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Glu Phe
          325   330   335

Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr
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Ala Ile Asp His Asn Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly
        355   360   365

His Phe Thr Glu Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys Lys
370   375   380

Gly Phe Asn Ala Asp Val Val Glu Tyr Val Gly Asp Phe Ile Lys Pro
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Ile Asn Lys Pro Met Tyr Lys Ile Tyr Thr Thr Leu Lys Lys Ile Lys
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41

Asp Lys Lys Lys
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